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SEQUENCE LISTING

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<120> Method For Accelerating The Rate of Mucociliary Clearance

<130> 98-736

<140> US 09/218,913 <141> 1998-12-22

<160> 105

<170> PatentIn version 3.1

<210> 1

<211> 179

<212> PRT

<213> Homo sapiens

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Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr 20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser 35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser 85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr 100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg 115 120 125 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn 130 135 140

The state of the second of the

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu Ala Gly
165 170 175

Ala Val Ser

<210> 2

<211> 197

<212> PRT

<213> Homo sapiens

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<221> SIGNAL

<222> (1)..(18)

<223>

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Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser 20 25 30

Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn 35 40 45

Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly 50 55 60

Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala 65 70 75 80

Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala 85 90 95

Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp 100 105 110 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala 115 120 125

Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val 130 135 140

Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn 145 150 155 160

Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg 165 170 175

Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu 180 185 190

Ala Gly Ala Val Ser 195

<210> 3

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3

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Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu 20 25 30

Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys 35 40 45

Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly 50 60

Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala 65 70 75 80

Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr 85 90 95

Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser 100 105 110 Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe 115 120 125

Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu 130 135 140

Ala Cys Met Leu Arg Cys Phe Arg Gln 145 150

<210> 4

<211> 58

<212> PRT

<213> Homo sapiens

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Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala 1 $$ 5 $$ 10 $$ 15

Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu 20 25 30

Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys 35 40 45

Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50

<210> 5

<211> 51

<212> PRT

<213> Homo sapiens

<400> 5

Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly 20 25 30

Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Lys Lys Cys

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<210> <211> 58 <212> PRT

<213> Homo sapiens

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Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn 20 25

Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu 40

Glu Ala Cys Met Leu Arg Cys Phe Arg Gln 50 55

<210> 7 <211> 51

<212> PRT

<213> Homo sapiens

<400> 7

Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg

Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly 20

Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met 40

Leu Arg Cys 50

<210> 8

<211> 92

<212> PRT

<213> Homo sapiens

<400> 8

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val

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| Val Gly Arg Cys 20 | Arg Ala Ser Met Pro 25 | Arg Trp Trp Tyr Asn 30 | Val Thr |
| Asp Gly Ser Cys 35 | Gln Leu Phe Val Tyr 40 | Gly Gly Cys Asp Gly 45 | Asn Ser |
| Asn Asn Tyr Leu 50 | Thr Lys Glu Glu Cys 55 | Leu Lys Lys Cys Ala 60 | Thr Val |
| Thr Glu Asn Ala 65 | Thr Gly Asp Leu Ala 70 | Thr Ser Arg Asn Ala 75 | Ala Asp 80 |
| Ser Ser Val Pro | Ser Ala Pro Arg Arg 85 | Gln Asp Ser 90 | |
| <210> 9 <211> 708 <212> DNA <213> Artificia | al Sequence | | |
| <220> <223> Consensus | s DNA sequence of hum | man Bikunin (Fig. 3). | |
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| <220> <221> misc_feat <222> (707)(7) <223> "n" is an | | | |
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| ccgagaacgc agcat | tccacg acttctgcct ggt | gtcgaag gtggtgggca g | matgccgggc 120 |
| ctccatgcct aggto | ggtggt acaatgtcac tga | eggatee tgecagetgt t | tgtgtatgg 180 |
| gggctgtgac ggaaa | acagca ataattacct gac | caaggag gagtgcctca a | gaaatgtgc 240 |
| cactgtcaca gagaa | atgcca cgggtgacct ggc | caccage aggaatgcag c | ggatteete 300 |
| tgtcccaagt gctcc | ccagaa ggcaggattc tgà | agaccac tccagcgata t | gttcaacta 360 |
| | | | |

tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcatcct tcccacgctg

| gtactttgac | gtggagagga | actcctgcaa | taacttcatc | tatggaggct | gccggggcaa | 480 |
|------------|------------|------------|------------|------------|------------|-----|
| taagaacagc | taccgctctg | aggaggcctg | catgctccgc | tgcttccgcc | agcaggagaa | 540 |
| tcctcccctg | ccccttggct | caaaggtggt | ggttctggcc | ggggctgttt | cgtgatggtg | 600 |
| ttgatccttt | tcctggggag | catccatggt | cttactgatt | ccgggtggca | aggaggaacc | 660 |
| aggagcgtgc | cctgcgganc | gtctggagct | tcggagatga | caagggnt | | 708 |
| | | | | | | |

<210> 10

<211> 197

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acids -18 to 179 of translation of consensus sequence in Fig. 3.

<400> 10

Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Ser Gly Val
1 5 10 15

Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser 20 25 30

Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn 35 40 45

Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly 50 55 60

Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala 65 70 75 80

Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala 85 90 95

Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
100 105 110

His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala 115 120 125

Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val 130 135 140

Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn 145 150 155 160

Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg 165 170 175

Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu 180 185 190

Ala Gly Ala Val Ser 195

<210> 11

<211> 179

<212> PRT

<213> Artificial Sequence

<220>

<223> Variants of human Bikunin.

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

<221> MISC_FEATURE

<222> (19)..(19)

<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

<221> MISC_FEATURE

<222> (21)..(26)

<223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa"

in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

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- <220>
- <221> MISC_FEATURE
- <222> (40)..(40)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC_FEATURE
- <222> (42)..(42)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC_FEATURE
- <222> (45)..(47)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC_FEATURE
- <222> (52)..(52)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC_FEATURE
- <222> (64)..(64)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).
- <220>
- <221> MISC_FEATURE
- <222> (103)..(103)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

- <221> MISC_FEATURE
- <222> (112)..(112)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

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<220>

- <221> MISC_FEATURE
- <222> (114)..(114)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

- <221> MISC_FEATURE
- <222> (116)..(121)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

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- <222> (135)..(135)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

- <221> MISC_FEATURE
- <222> (137)..(137)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

- <221> MISC_FEATURE
- <222> (140)..(142)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<220>

<221> MISC_FEATURE

- <222> (147)..(147)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

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- <220>
- <221> MISC_FEATURE
- <222> (159)..(159)
- <223> Each "Xaa" independently represents a naturally occurring amino acid residue except Cys, with the proviso that at least one "Xaa" in SEQ ID NO:11 is different from the corresponding amino acid residue of the native sequence (see page 10 of specification).

<400> 11

- Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val 1 5 10 15
- Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr
 20 25 30
- Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser 35 40 45
- Asn Asn Tyr Xaa Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Xaa 50 60
- Thr Glu Asn Ala Thr Gly Asp Leu Ser Thr Ser Arg Asn Ala Ala Asp 65 70 75 80
- Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu His Asp Ser 85 90 95
- Ser Asp Met Phe Asn Tyr Xaa Glu Tyr Cys Thr Ala Asn Ala Val Xaa 100 105 110
- Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Trp Tyr Phe Asp Val Glu Arg
- Asn Ser Cys Asn Asn Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Lys Asn 130 135 140
- Ser Tyr Xaa Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Xaa Gln 145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly 165 170 175

Ala Val Ser

| <210><211><212><212><213> | | |
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| | <pre>misc_feature (384)(384) "n" is any nucleotide.</pre> | |
| | <pre>misc_feature (390)(390) "n" is any nucleotide.</pre> | |
| <400> | 12 gteg tttetegeet ggetgggate getgeteete tetggggtee tggeeggeeg | 60 |
| | aacg cagcatccac gacttctgcc tggtgtcgaa ggtggtgggc agattccggg | 120 |
| | tgcc taggtggtgg tacaatgtca ctgacggatc ctgccagctg tttgtgtatg | 180 |
| | gtga cggaaacagc aataattacc tgaccaagga ggagtgcctc aagaaatgtg | 240 |
| | tcac agagaatgcc acgggtgacc tggccaccag caggaatgca gcggattcct | 300 |
| ctgtcc | caag tgctcccaga aggcaggatt cttgaagacc acttcagcga tatgtttcaa | 360 |
| ntattg | naag aataattgca ccgncaacgn att | 393 |
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Trp Pro Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
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                               25
Lys Val Val Gly Arg Glu Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
       35
                           40
Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
   50
                       55
Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
65
                   70
                                       75
Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
           100
                               105
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<211> 510
<212> DNA
<213> Homo sapiens
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<223> "n" is any nucleotide.
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<222> (481)..(481)
<223> "n" is any nucleotide.
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<213> Homo sapiens

<222> (509)..(509) <223> "n" is any nucleotide. <400> 14 gcaataatta cctgaccaag gaggagtgcc tcaagaaatg tgccactgtc acagagaatg 60 ccacgggtga cctggccacc agcaggaatg cagcggattc ctctgtccca agtctcccag 120 aaggcaggat totgaagaco actocagoga tatgttcaac tatgaagaat actgcacogo 180 caacgcagtc actgggcctt gccgtgcatc cttcccacgc tggtactttg acgtggagag 240 gaactcctgc aataacttca tctatggagg ctgccggggc aataagaaca gctaccgctc 300 tgaggaggcc tgcatgctcc gctgcttccg ccagcaggag aatcctcccc tgccccttgg 360 ctcaaaggtg gtggttctgg ccggggctgt ttcgtgatgg tgttgatcct tttcctgggg 420 agentecatg gtettactga tteegggtgg caaggaggaa ecaggagegt geeetgegga 480 ncgtctggag cttcggagat gacaagggnt 510 <210> 15 <211> 20 <212> PRT <213> Homo sapiens <400> 15 Leu Pro Asp Gln Gly Gly Val Pro Gln Glu Met Cys His Cys His Arg 10 Glu Cys His Gly 20 <210> 16 <211> 427 <212> DNA <213> Homo sapiens <220> <221> misc_feature <222> (3)..(3) <223> "n" is any nucleotide. <220> <221> misc_feature <222> (11)..(12)<223> "n" is any nucleotide.

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<222> (17)..(17)
<223> "n" is any nucleotide.
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<222> (48)..(48)
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      (425)..(425)
<223> "n" is any nucleotide.
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agaacgcagc atccacgact tctgcctggt gtcgaaggtg gtgggcagat gccgggcctc
                                                                     120
catgcctagg tggtggtaca atgtcactga cggatcctgc cagctgtttg tgtatggggg
                                                                     180
ctgtgacgga aacagcaata attacctgac caaggaggag tgcctcaaga aatgtgccac
                                                                     240
tgtcacagag aatgccacgg gtgacctggc caccagcagg aatgcagcgg attcctctgt
                                                                     300
cccaagtgct cccagaaggc aggattctga agaccactcc agcgatatgt tcaactatga
                                                                     360
agaatactgg caccgccaac gcattcactg ggcctgcgtg catccttccc acgctggtac
                                                                     420
tttgncg
                                                                     427
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<211> 423
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<222> (6)..(6)
<223> "n" is any nucleotide.
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      (407)..(407)
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<223> "n" is any nucleotide.

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Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe

Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe 20 25 30

Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln 35 40 45

Glu Cys Leu Arg Ala Cys Lys Lys Gly
50 55

5

<210> 21 <211> 57 <212> PRT <213> Unknown

<220> <223>

<400> 21
Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu

Leu Leu Arg Tyr Tyr Tyr Arg Tyr Arg Thr Gln Ser Cys Arg Gln Phe 20 25 30

Kunitz-like domain of tissue factor pathway inhibitor precursor 2.

15

10

Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu 40 Ala Cys Asp Asp Ala Cys Trp Arg Ile <210> 22 <211> 57 <212> PRT <213> Unknown <220> <223> Kunitz-like domain of tissue factor pathway inhibitor precursor 2. <400> 22 Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr Cys Asp Ala Phe 25 20 Thr Tyr Thr Gly Cys Gly Asn Asn Asn Asn Phe Val Ser Arg Glu 35 40 Asp Ser Lys Arg Ala Cys Ala Lys Ala 50 55 <210> 23 <211> 57 <212> PRT <213> Unknown <220> <223> Kunitz-like domain of amyloid precursor protein homologue. <400> 23 Lys Ala Val Cys Ser Gln Glu Ala Met Thr Gly Pro Cys Arg Ala Val Met Pro Arg Thr Thr Phe Asp Leu Ser Lys Gly Lys Cys Val Arg Phe 20 25

The state of the same of the same

45

Ile Thr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Glu Ser Glu Asp

40

35

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Tyr Cys Met Ala Val Cys Lys Ala Met
    50
<210> 24
<211> 58
<212> PRT
<213> Unknown
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<223> Kunitz-like domain of aprotinin.
<400> 24
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Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
                                25
Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys Ser Ala
Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
<210> 25
<211> 51
<212> PRT
<213> Unknown
<220>
<223> Kunitz-like domain of inter-alpha-trypsin inhibitor precursor.
<400> 25
Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys Met Gly Met Thr Ser Arg
Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys Glu Thr Phe Gln Tyr Gly
            20
Gly Cys Met Gly Asn Gly Asn Asn Phe Val Thr Glu Lys Glu Cys Leu
Gln Thr Cys
    50
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<210> 26

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<211> 57 <212> PRT
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<213> Unknown

<220>

<223> Kunitz-like domain of inter-alpha-trypsin inhibitor precursor.

<400> 26

Val Ala Ala Cys Asn Leu Pro Ile Val Arg Gly Pro Cys Arg Ala Phe 1 5 10 15

Ile Gln Leu Trp Ala Phe Asp Ala Val Lys Gly Lys Cys Val Leu Phe 20 25 30

Pro Tyr Gly Gly Cys Gln Gly Asn Gly Asn Lys Phe Tyr Ser Glu Lys 35 40 45

Glu Cys Arg Glu Tyr Cys Gly Val Pro 50 55

<210> 27

<211> 57

<212> PRT

<213> Unknown

<220>

<223> Kunitz-like domain of amyloid precursor protein.

<400> 27

Glu Val Cys Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met 1 5 10 15

Ile Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe 20 25 30

Phe Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu 35 40 45

Tyr Cys Met Ala Val Cys Gly Ser Ala 50 55

<210> 28

<211> 51

<212> PRT

<213> Unknown

<220>

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<223> Kunitz-like domain of collagen alpha-3(VI) precursor.
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Cys Lys Leu Pro Lys Asp Glu Gly Thr Cys Arg Asp Phe Ile Leu Lys
Trp Tyr Tyr Asp Pro Asn Thr Lys Ser Cys Ala Arg Phe Trp Tyr Gly
Gly Cys Gly Gly Asn Glu Asn Lys Phe Gly Ser Gln Lys Glu Cys Glu
                            40
Lys Val Cys
    50
<210> 29
<211> ·57
<212> PRT
<213> Unknown
<220>
<223> Kunitz-like domain of HKI-B9.
<400> 29
Pro Asn Val Cys Ala Phe Pro Met Glu Lys Gly Pro Cys Gln Thr Tyr
Met Thr Arg Trp Phe Phe Asn Phe Glu Thr Gly Glu Cys Glu Leu Phe
            20
                                25
Ala Tyr Gly Gly Cys Gly Gly Asn Ser Asn Asn Phe Leu Arg Lys Glu
        35
                            40
Lys Cys Glu Lys Phe Cys Lys Phe Thr
    50
<210> 30
<211> 46
<212> DNA
<213> Artificial Sequence
<223> 5' sense oligonucleotide used in Example 6.
```

gccaagcttg gataaaagat atgaagaata ctgcaccgcc aacgca

46

```
<210> 31
<211> 35
<212>
      DNA
<213> Artificial Sequence
<220>
<223>
      3' antisense oligonucleotide used in Example 6.
<400> 31
                                                                      35
ggggatcctc actgctggcg gaagcagcgg agcat
<210>
      32
      206
<211>
<212> DNA
<213> Artificial Sequence
<220>
<223> Cloned bikunin cDNA fragment in Example 6.
<400> 32
ccaagcttgg ataaaagata tgaagaatac tgcaccgcca acgcagtcac tgggccttgc
                                                                     60
cgtgcatcct tcccacgctg gtactttgac gtggagagga actcctgcaa taacttcatc
                                                                     120
tatggaggct gccggggcaa taagaacagc taccgctctg aggaggcctg catgctccgc
                                                                     180
tgcttccgcc agcagtgagg atcccc
                                                                     206
<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence
<220>
<223> 3' PCR primer used to amplify EST R74593.
<400> 33
                                                                      28
cgaagcttca tctccgaagc tccagacg
<210>
      34
<211>
      31
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' PCR primer used to amplify EST R74593.
<400> 34
                                                                      31
aggatctaga caataattac ctgaccaagg a
<210> 35
```

A Day of the second of the second of

<211> 37

```
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' PCR primer used to amplify EST R35464.
<400> 35
ggtctagagg ccgggtccgt ttctcgcctg gctggga
                                                                      37
<210> 36
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' PCR primer used to amplify EST R34808.
<400> 36
cacctgatcg cgagacccc
                                                                      19
<210> 37
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Vector specific DNA sequencing primer (SP6).
<400> 37
                                                                      19
gatttaggtg acactatag
<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Vector specific DNA sequencing primer (T7).
<400> 38
taatacgact cactataggg
                                                                      20
<210> 39
<211>
      22
<212> DNA
<213> Artificial Sequence
<220>
<223> Gene specific DNA sequencing primer.
<400> 39
ttacctgacc aaggaggagt gc
                                                                      22
```

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```
<210> 40
<211>
      23
<212> DNA
<213> Artificial Sequence
<220>
<223> Gene specific DNA sequencing primer.
<400> 40
                                                                      23
aatccgctgc attcctgctg gtg
<210> 41
<211>
       20
<212>
      DNA
<213> Artificial Sequence
<220>
<223>
      Gene specific DNA sequencing primer.
<400> 41
cagtcactgg gccttgccgt
                                                                      20
<210> 42
<211> 105
<212>
      DNA
<213> Artificial Sequence
<220>
<223> 5' sense oligonucleotide used in Example 5.
<400> 42
gaaggggtaa gcttggataa aagatatgaa gaatactgca ccgccaacgc agtcactggg
                                                                      60
ccttgccgtg catccttccc acgctggtac tttgacgtgg agagg
                                                                     105
<210> 43
<211>
      129
<212> DNA
<213> Artificial Sequence
<220>
<223>
      3' antisense oligonucleotide used in Example 5.
<400> 43
cgcggatccc tactggcgga agcagcggag catgcaggcc tcctcagagc ggtagctgtt
                                                                     60
cttattgccc cggcagcctc catagatgaa gttattgcag gagttcctct ccacgtcaaa
                                                                     120
gtaccagcg
                                                                     129
<210> 44
```

<211> 207

```
<212> DNA
<213> Artificial Sequence
<220>
<223> Cloned bikunin fragment in Example 5.
<400> 44
gaaggggtaa gcttggataa aagatatgaa gaatactgca ccgccaacgc agtcactggg
                                                                       60
ccttgccgtg catccttccc acgctggtac tttgacgtgg agaggaactc ctgcaataac
                                                                      120
ttcatctatg gaggctgccg gggcaataag aacagctacc gctctgagga ggcctgcatg
                                                                      180
ctccgctgct tccgccagta gggatcc
                                                                      207
<210> 45
<211> 248
<212> PRT
<213> Artificial Sequence
<220>
<223>
      EST derived consensus sequence of human Bikunin (Figs. 4D and 4G).
<220>
      SIGNAL
<221>
<222>
      (1)..(23)
<223>
<400> 45
Met Leu Arg Ala Glu Ala Asp Gly Val Ser Arg Leu Leu Gly Ser Leu
Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp
            20
Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro
        35
                            40
                                                 45
Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr
    50
                        55
                                            60
Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys
65
                    70
                                        75
                                                             80
Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala
                                    90
                85
                                                         95
```

Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg

105 100 110

Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr 115 120

Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg 130 135

Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly 145 150 155 160

Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met 170

Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser

Lys Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe 200 205

Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln 210 215 220

Glu Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln 225 230 235

Leu Val Lys Asn Thr Tyr Val Leu 245

<210> 46

<211> 782

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (61)..(780)

<223>

<400> 46

acctgatege gagaceceaa eggetggtgg egtegeetge gegtetegge tgagetggee

60 108

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atg gcg cag ctg tgc ggg ctg agg cgg agc cgg gcg ttt ctc gcc ctg Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu 5 10

| | | | | | tct Ser | | | | | | | | | | 156 |
|----|-------|---|-------------|-----|-------------------|-----|---|-----|-----|---|---|---|---|---|-----|
| | | | | | ctg Leu | | | | | | | | | | 204 |
| | | | | | tgg Trp 55 | | | | | | | | | | 252 |
| | | | | | tgt Cys | | | | _ | | | | _ | | 300 |
| _ | - | _ | | _ | aaa Lys | _ | _ | | - | | | | _ | ~ | 348 |
| | _ | _ | | | agg Arg | | _ | | - | | | - | | - | 396 |
| | | | | | tct Ser | | | | | _ | _ | _ | | | 444 |
| | | | | | gcc Ala 135 | | | | | | | | | | 492 |
| | | | | | ttt Phe | | | | | | | | | | 540 |
| | Tyr | | ${\tt Gly}$ | Cys | cgg Arg | Gly | | Lys | Asn | | | | | | 588 |
| | | | | | tgc Cys | | | | | | | | | | 636 |
| | | | | | gtg Val | | | | | | | | | | 684 |
| | | | | | gcc Ala 215 | | | | | | | | | | 732 |
| | | | | | gcc Ala | | | | | | | | | | 780 |
| ga | | | | | | | | | | | | | | | 782 |

<211> 240 <212> PRT <213> Homo sapiens <220> <221> SIGNAL <222> (1)..(27) <223> <400> 47 Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg 40 45 Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln 50 55 Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr 70 75 Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr 85 90 Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn 115 120 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala 130 135 140 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn 145 150 155 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu 165 170

water the set the set to

<210> 47

Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu 180 Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly Leu Phe Val Met Val 200 Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Phe Gly Asp 230 235 <210> 48 <211> 1544 <212> DNA <213> Homo sapiens <220> <221> misc_feature <222> (1358)..(1358) <223> "n" is any nucleotide. <220> <221> exon <222> (301)..(1056)<223> <400> 48 gcacgagttg ggaggtgtag cgcggctctg aacgcgctga gggccgttga gtgtcgcagg 60 120 cggcgagggc gcgagtgagg agcagaccca ggcatcgcgc gccgagaagg ccgggcgtcc ccacactgaa ggtccggaaa ggcgacttcc gggggctttg gcacctggcg gaccctcccg 180 gagcgtcggc acctgaacgc gaggcgctcc attgcgcgtg cgcgttgagg ggcttcccgc 240 acctgatege gagaceceaa eggetggtgg egtegeetge gegtetegge tgagetggee 300 atg gcg cag ctg tgc ggg ctg agg cgg agc cgg gcg ttt ctc gcc ctg 348 Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu 10 ctg gga tcg ctg ctc ctc tct ggg gtc ctg gcg gcc gac cga gaa cgc 396 Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg 20 25 agc atc cac gac ttc tgc ctg gtg tcg aag gtg gtg ggc aga tgc cgg 444 Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg 35 40 45

| _ | | _ | | | | tgg Trp 55 | | | - | | _ | | | _ | 5 | | 492 |
|------|-------|-------|-------|------|-------|-------------------|------|-------|-------|------|------|-------|-------|-------|-------|---|------|
| | | | | | | tgt Cys | | | | | | | | | | | 540 |
| _ | | | - | | _ | aaa Lys | _ | _ | | _ | | | | ~ | _ | | 588 |
| | - | _ | _ | | - | agg Arg | | - | | - | | | _ | | - | | 636 |
| | | | | | | tct Ser | | | | - | | - | - | | | | 684 |
| | | | | | | gcc Ala 135 | | | | | | | | | | | 732 |
| | | | | | | ttt Phe | | | | | | | | | | | 780 |
| | | | | | | cgg Arg | | | | | | | | | | | 828 |
| | | | | | | tgc Cys | | | | | | | | | _ | | 876 |
| | | | | | | gtg Val | | | | | | | | | | | 924 |
| | | | | | | gcc Ala 215 | | | | | | | | | | | 972 |
| | | | | | | gcc Ala | | | | | | | | | | | 1020 |
| | | | | | | aag Lys | | | | _ | _ | tgad | ceged | cct | | | 1066 |
| gtc | gccaa | aga g | ggact | gggg | ja aç | ggag | ggga | a gad | ctato | gtgt | gago | etttt | tt t | caaat | agag | g | 1126 |
| gatt | gact | cg g | gattt | gagt | gat | catt | aggg | gctg | gaggt | ctg | tttc | ctcto | igg a | aggta | aggac | g | 1186 |

<210> 49

<211> 252

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> (1)..(27)

<223>

<400> 49

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu 1 5 10 15

Leu Gly Ser Leu Leu Ser Gly Val Leu Ala Ala Asp Arg Glu Arg 20 25 30

Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg 35 40 45

Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln 50 55 60

Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr 65 70 75 80

Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr 85 90 95

Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser 100 105 110

Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn 115 120 125

Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala 135 140 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn 150 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu 170 Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Glu Asn Pro Pro Leu 185 Pro Leu Gly Ser Lys Val Val Leu Ala Gly Leu Phe Val Met Val 200 Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala 215 Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp 225 230 235 Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val Leu 245 250 <210> 50 <211> 146 <212> PRT <213> Homo sapiens <400> 50 Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg 10 Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly 20 Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu

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Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln

Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr

35

50

| 65 | | | | 70 | | | | | 75 | | | | | 80 |
|----------------------------------|---------------------------------------------------------|------------|-----------|-------|------------|------------|------------|-----------|-------|------------|------------|------------|-----------|-----|
| Asp Se | er Glu | Asp | His 85 | Ser | Ser | Asp | Met | Phe 90 | Asn | Tyr | Glu | Glu | Tyr 95 | Cys |
| Thr Al | a Asn | Ala 100 | Val | Thr | Gly | Pro | Cys 105 | Arg | Ala | Ser | Phe | Pro 110 | Arg | Trp |
| Tyr Ph | e Asp 115 | Val | Glu | Arg | Asn | Ser 120 | Cys | Asn | Asn | Phe | Ile 125 | Tyr | Gly | Gly |
| Cys Ar | | Asn | Lys | Asn | Ser 135 | Tyr | Arg | Ser | Glu | Glu 140 | Ala | Cys | Met | Leu |
| Arg Cys 145 | | | | | | | | | | | | | | |
| <210><211><211><212><213> | | ficia | al Se | equer | nce | | | | | | | | | |
| <220> <223> | Conse | ensus | s bi} | cunir | ı sed | quenc | ce of | E Fig | g. 40 | c. | | | | |
| <220><221><222><222><223> | <pre>misc_feature (46)(46) "n" is any nucleotide.</pre> | | | | | | | | | | | | | |
| <220> <221> <222> <223> | misc_ (117) "n" i |)(1 | 17) | ıcled | otide | ∍. | | | | | | | | |
| <220> <221> <222> | 221> misc_feature | | | | | | | | | | | | | |

<400> 51
gcgacctccg cgcgttggga ggtgtagcgc ggctctgaac gcgtgnaggg ccgttgagtg 60
tcgcaggcgg cgagggcgcg agtgaggagc agacccaggc atcgcgcgc gagaagncgg 120
gcgtccccac actgaaggtc cggaaaggcg acttccgggg gctttggcac ctggcggacc 180
ctcccggagc gtcggcacct gaacgcgagg cgctccattg cgcgtgcgtt tgaggggctt 240

<223> "n" is any nucleotide.

cccgcacctg atcgcgagac cccaacggct ggtggcgtcg ctgcgcgtct cggctgagct 300 ggccatggcg cantgttgcg ggctgaggcg gacggcgttt ctcgcctgct gggatcgctg 360 ctcctctctg gggtcctggc ggccgaccga gaacgcagca tccacgactt ctgcctggtg 420 tcgaaggtgg tgggcagatg ccgggcctcc atgcctaggt ggtggtacaa tgtcactgac 480 ggatcctgcc agctgtttgt gtatgggggc tgtgacggaa acagcaataa ttacctgacc 540 aaggaggagt gcctcaagaa atgtgccact gtcacagaga atgccacggg tgacctggcc 600 accagcagga atgcagcgga ttcctctgtc ccaagtgctc ccagaaggca ggattctgaa 660 gaccactcca gcgatatgtt caactatgaa gaatactgca ccgccaacgc agtcactggg 720 cettgeegtg cateetteec acgetggtae tttgaegtgg agaggaacte etgeaataae 780 ttcatctatg gaggctgccg gggcaataag aacagctacc gctctgagga ggcctgcatg 840 ctccgctgct tccgccagca ggagaatcct cccctgcccc ttggctcaaa ggtggtggtt 900 ctggcggggc tgttcgtgat ggtgttgatc ctcttcctgg gagcctccat ggtctacctg 960 atccgggtgg cacggaggaa ccaggagcgt gccctgcgca ccgtctggag ctccggagat 1020 gacaaggage agetggtgaa gaacacatat gteetgtgae egeeetgteg eeaagaggae 1080 tggggaaggg aggggagact atgtgtgagc tttttttaaa tagagggatt gactcggatt 1140 tgagtgatca ttagggctga ggtctgtttc tctgggaggt aggacggctg cttcctggtc 1200 tggcagggat gggtttgctt tggaaatcct ctaggaggct cctcctcgca tggcctgcag 1260 tctggcagca gccccgagtt gtttcctcgc tgatcgattt ctttcctcca ggtagagttt 1320 tetttgetta tgttgaatte cattgeetet ttteteatea eagaagtgat gttggaateg 1380 tttcttttgt ttgtctgatt tatggttttt ttaagtataa acaaaagttt tttattagca 1440 ttctgaaaga aggaaagtaa aatgtacaag tttaataaaa aggggccttc ccctttagaa 1500 taaaaaaaa aaaaaaaaa aaaaaaaaa 1530 A CONTRACT SERVE

```
<210> 52
<211> 170
<212> PRT
```

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val 1 5 10 15

<213> Homo sapiens

<400> 52

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr 20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser 35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser 85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg 115 120 125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn 130 135 140

Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln 145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys 165 170

<210> 53

<211> 27

<212> PRT

<213> Homo sapiens

<400> 53

Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu Ala Leu 1 5 10 15

Leu Gly Ser Leu Leu Ser Gly Val Leu Ala 20 25

<210> 54

<211> 23

```
<400> 54
Met Leu Arg Ala Glu Ala Asp Gly Val Ser Arg Leu Leu Gly Ser Leu
                                 10
Leu Leu Ser Gly Val Leu Ala
           20
<210> 55
<211>
      102
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' sense oligonucleotide used for construct #2 in Example 5.
<400> 55
60
tgtagagctt cttttccaag atggtacttt gatgttgaaa ga
                                                                102
<210> 56
<211> 129
<212> DNA
<213> Artificial Sequence
<220>
<223>
     3' antisense oligonucleotide used for construct #2 in Example 5.
<400> 56
actggatcct cattggcgaa aacatctcaa catacaggct tcttcagatc tgtaagaatt
tttattacct ctacaaccac cgtaaataaa attattacaa gaatttcttt caacatcaaa
                                                                120
gtaccatct
                                                                129
<210> 57
<211> 108
<212> DNA
<213> Artificial Sequence
<220>
<223> 5' sense oligonucleotide used for construct #3 in Example 5.
<400> 57
gaaggggtaa gcttggataa aagaaattac gaagaatact gtactgctaa tgctgttact
                                                                 60
ggtccatgta gagcttcttt tccaagatgg tactttgatg ttgaaaga
                                                                108
```

<212> PRT

<213> Homo sapiens

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<210> 58
<211> 117
<212> DNA
<213> Artificial Sequence
<220>
<223>
      5' sense oligonucleotide used for construct #4 in Example 5.
<400> 58
gaaggggtaa gcttggataa aagagatatg tttaattacg aagaatactg tactgctaat
                                                                     60
gctgttactg gtccatgtag agcttctttt ccaagatggt actttgatgt tgaaaga
                                                                    117
<210> 59
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> Sense oligonucleotide used in PCR in Example 8.
<400> 59
cacctgatcg cgagacccc
                                                                      19
<210> 60
<211>
      23
<212> DNA
<213> Artificial Sequence
<220>
<223>
      Antisense oligonucleotide used in PCR in Example 8.
<400> 60
ctggcggaag cagcggagca tgc
                                                                      23
<210> 61
<211>
      45
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide used in in vitro mutagenesis in Example 9.
<400> 61
cgcgtctcgg ctgacctggc cctgcagatg gcgcacgtgt gcggg
                                                                     45
<210> 62
<211> 60
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide used in in vitro mutagenesis in Example 9.
```

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```
<400> 62
ctgccccttg gctcaaagta ggaagatctt cccccgggg gggtggttct ggcggggctg
                                                                     60
<210> 63
<211> 14
<212> PRT
<213> Homo sapiens
<400> 63
Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Pro Leu Gly
                                   10
<210> 64
<211> 20
<212> PRT
<213> Homo sapiens
<400> 64
Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
                                   10
Val Gly Arg Cys
           20
<210> 65
<211> 20
<212> PRT
<213> Homo sapiens
<400> 65
Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys
1
                                   10
Arg Ala Ser Phe
           20
<210> 66
<211>
      11
<212>
      PRT
<213> Homo sapiens
<400> 66
Pro Arg Tyr Val Asp Gly Ser Gln Phe Tyr Gly
```

```
<210> 67
<211> 55
<212> PRT
<213> Homo sapiens
<400> 67
Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
                                   10
Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu
                               25
Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu
Val Lys Asn Thr Tyr Val Leu
<210> 68
<211> 43
<212> PRT
<213> Homo sapiens
<400> 68
Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
                                   10
Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu
                               25
Arg Ala Leu Arg Thr Val Trp Ser Phe Gly Asp
<210> 69
<211> 55
<212> PRT
<213> Homo sapiens
<400> 69
Val Val Leu Ala Gly Leu Phe Val Met Val Leu Ile Leu Phe Leu
                                   10
```

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Gly Ala Ser Met Val Tyr Leu Ile Arg Val Ala Arg Arg Asn Gln Glu

25

Arg Ala Leu Arg Thr Val Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu $35 \hspace{1cm} 40 \hspace{1cm} 45$

Val Lys Asn Thr Tyr Val Leu 50 55

<210> 70

<211> 213

<212> PRT

<213> Homo sapiens

<400> 70

Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val 1 5 10 15

Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser 35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser 85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr 100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg 115 120 125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn 130 135 140

Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln 145 150 155 160

Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly 165 170 175

Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr 180 185 190

Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val 195 200 205

Trp Ser Phe Gly Asp 210

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<211> 225

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Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr 20 25 30

Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser 35 40 45

Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val 50 55 60

Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp 65 70 75 80

Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser 85 90 95

Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr 100 105 110

Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg 115 120 125

Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn 130 135 140

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Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
145
                    150
                                        155
Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Leu Ala Gly
                                   170
Leu Phe Val Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr
            180
                                185
Leu Ile Arg Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val
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Trp Ser Ser Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val
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Leu
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10

Xaa Thr Xaa

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<213> Homo sapiens

<400> 73

Pro Gly His Gln Gln Glu Cys Ser Gly Phe Leu Cys Pro Lys Ser Pro 1 5 10 15

Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr Glu 20 25 30

Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe 35 40 45

Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile 50 55 60

Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala 65 70 75 80

Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro Pro Leu Pro Leu 85 90 95

Gly Ser Lys Val Val Leu Ala Gly Ala Val Ser 100 105

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1 5 10 15

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                                                                      120
gaaggcagga ttctgaagac cactccagcg atatgttcaa ctatgaagaa tactgcaccg
                                                                      180
ccaacgcagt cactgggcct tgccgtgcat ccttcccacg ctggtacttt gacgtggaga
                                                                      240
ggaactcctg caataacttc atctatggag gctgccgggg caataagaac agctaccgct
                                                                      300
ctgaggaggc ctgcatgctc cgctgcttcc gccagcagga gaatcctccc ctgccccttg
                                                                      360
gctcaaaggt ggtggttctg gccggggctg tttcgtgatg gtgttgatcc ttttcctggg
                                                                      420
gagenteeat ggtettaetg atteegggtg geaaggagga accaggageg tgeeetgegg
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ancgtctgga gcttcggaga tgacaagggn t
                                                                      511
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<211>

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31

PRT

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Glu Glu Pro Gly Ala Cys Pro Ala Xaa Arg Leu Glu Leu Arg Arg
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gtcgcaggcg gcgagggcgc gagtgaggag cagacccagg catcgcgcgc cgagaagncg
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Metat

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ggcgtcccca cactgaaggt ccggaaaggc gacttccggg ggctttggca cctggcggac
                                                                     180
cctcccggag cgtcggcacc tgaacgcgag gcgctccatt gcgcgtgcgt ntgaggggct
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teeegeacet gategegaga eeceaaegge tggtggegte geetgegegt eteggetgag
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                                                                     120
genteceeae actgaaggte eggaaaggeg actteegggg getttggeae etggeggaee
                                                                     180
ctcccggagc gtggcacctg aacgcgaggc gctccattgc gcgtgcgttt gaggggcttc
                                                                     240
ccgcacctga tcgcgagacc ccaacggctg gtggcgtcgc ctgcgcgtct cggctgagct
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ggccatggcg cactgtgcgg ngctgaggcg
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Sea Carlow Market

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                                                                    120
ggcggaccet cccggagcgt cggcacctga acgcgaggcg ctccattgcg cgtgcgtttg
                                                                    180
aggggettee egeacetgat egegagaeee caaeggetgg tngcgteget negegteteg
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gctgagcttg gccatggcgc antgttncgg gctnaggcgg acg
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tccccacact gaaggtccgg aaaggcgact tccgggggct ttggcacctg gcggacgtcc
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cggagcnggc acctgaacgc gaggcgctcc attgcgcgtg cgtttgaggg gcttcccgca
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cctgatcgcg agaccccaac ggctggtngc gtcgctggcg cgttctcggc tgagctggcc
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atggcgcant gttgcgngct gaggcggacc gncgtttttc ttcgccttgc tgggattcgc
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ttgcttcctn tctgggggtt cctgggcggc cgaccgagaa cgcagcatcc aagaattttt
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gaaaggcgac ttccgggggc tttggcacct ggcggaccct cccggagcgt cggcacctga
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acgcgaggcg ctccattgcg cgtgcgtntg gaggggcttc ccgcacctga tcgcgagacc
                                                                     180
ccaacggctg gtgggcgtcg ctgcgcgtct tcggctgagc tgggccatgg cgcanttgtt
                                                                     240
gegggetgag geggaegegg negtttttte gneettgetg ggattegttg tinetetetn
ggggttctgg ggnggccgan cgagaacgca agcattcacg attt
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                                                                    120
agctggccat ggcgcantgt tgcgngctga ggcggcggnc gttttctcgc ctgctgggat
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cgctgctcct ctctggggtc ctggcggccg accgagaacg cagcatccac ganttcttcc
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tggtgttcga agg
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tgaggagcag acccaggcat cgcgcgcga gaagncgggc gtccccacac tgaaggtccg
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gaaaggcgac ttccgggggc tttggcacct ggcggaccct cccggagcgt cggcacctga
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acgcgaggcg ctccattgcg cgtgcgtttg aggggcttcc cgcacctgat cgcgagaccc
                                                                     240
caacggctgg tggcgtcgcc tgcgcgtctc ggctgagctg gccatggcgc antggtgcgg
                                                                     300
gcttgaggcg gannngccgt ttctcgcctg ctgggatcgc tgctcctctc tggggtcctg
                                                                     360
gcggccgacc gagaacgcag catccacgac ttctgcctgg tgtcgaaggt ggtgggcag
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acttccgggg gctttggcac ctggcggacc ctcccggagc gtcggcacct gaacgcgagg
                                                                     120
cctccattgc cgtgcgttng aggggcttcc cggaacttga tcgcgagacc ccaacggctg
                                                                     180
gtggcgtcgc tgcgcgtcct cggctgagct ggccatggcg cantggtgcc gngctgaggc
                                                                     240
cggagggccg gtttctcgcc ttgctgggat cgctgctcct ctctgggggtc ctggcggccg
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ancgaagaan gcagcaatcc angaattnct gcctggtgtt cgaaagttgg tgggcanatt
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ccggggcctt catgnctaag gttggttggt anaatgtnaa ttaangattc ttgcaactgt
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accgagaacg cagcatccac gacttctgcc tggtgtcgaa ggtggtgggc agattccggg
                                                                     120
cctccatgcc taggtggtgg tacaatgtca ctgacggatc ctgccagctg tttgtgtatg
                                                                     180
ggggctgtga cggaaacagc aataattacc tgaccaagga ggagtgcctc aagaaatgtg
                                                                     240
ccactgtcac agagaatgcc acgggtgacc tggccaccag caggaatgca gcggattcct
                                                                     300
ctgtcccaag tgctcccaga aggcaggatt cttgaagacc acttcagcga tatgtttcaa
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ntattgnaag aataattgca ccgncaacgn att
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catgcctagg tggtggtaca atgtcactga cggatcctgc cagctgtttg tgtatggggg
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ctgtgacgga aacagcaata attacctgac caaggaggag tgcctcaaga aatgtgccac
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tgtcacagag aatgccacgg gtgacctggc caccagcagg aatgcagcgg attcctctgt
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cccaagtgct cccagaaggc aggattctga agaccactcc agcgatatgt tcaactatga
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caatgtcact gacggatect gecagetgtt tgtgtatggg ggetgtgacg gaaacagcaa
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taattacctg accaaggagg agtgcctcaa gaaatgtgcc actgtcacag agaatgccac
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gggtgacctg gccaccagca ggaatgcagc ggattcctct gtcccaagtg ctcccagaag
                                                                     300
gcaggattct gaagaccact ccagcgatat gttcaactat gaagaatact gcaccgccaa
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cgcagtcact ggggccttgc gtggaatcct ttcccacgct ggnaatttng acgttgagaa
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ggaac
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                                                                     120
ctctgtccca agtgctccca gaaggcagga ttctgaagac cactccagcg atatgttcaa
                                                                     180
ctatgaagaa tactgcaccg ccaacgcagt ncactgggcc ttgcgtggca tnccttccca
                                                                     240
cgctngtact ttgacgtgga gaggaactcc tggcaataac ttcatctatg gaggcttgcc
                                                                     300
ggggcaatna agaacagntt accgctcttt aggaggcctg cat
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                                                                     120
aaggcaggat totgaagaco actocagoga tatgttcaac tatgaagaat actgcacogo
                                                                     180
caacgcagtc actgggcctt gccgtgcatc cttcccacgc tggtactttg acgtggagag
                                                                     240
gaactcctgc aataacttca tctatggagg ctgccggggc aataagaaca gctaccgctc
                                                                     300
tgaggaggcc tgcatgctcc gctgcttccg ccagcaggag aatcctcccc tgccccttgg
                                                                     360
ctcaaaggtg gtggttctgg ccggggctgt ttcgtgatgg tgttgatcct tttcctgggg
                                                                     420
agentecatg gtettaetga tteegggtgg caaggaggaa eeaggagegt geeetgegga
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ncgtctggag cttcggagat gacaagggnt
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tgccccttgg ctcaaaggtg gtggttctgg cggggctgtt cgtgatggtg ttgatcctct
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tcctggggag cctccatggt ctacctgatc cgggtggcac ggagggaacc agggagcgtg
                                                                     180
ccctgcgcac cgtctgggag ctccggagat gacaagggag cagctgggtg aagaacacat
                                                                     240
atgttcctgt tgaccgncct gttcgccaag aggattgggg gaagggaggg gga
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                                                                     120
tccgggtggc acggaggaac ccaggancgt gccctgcgca ccgtctggag ctccggagat
                                                                     180
gacaaggagc agctggtgaa gaacacatat gtcctgtgac cgccctgtcg ccaagaggac
                                                                     240
tggggaaggg aggggagact atgtgtgagc tttttttaaa ta
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59

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gctctgagga ggcctgcgtg ctccgctgct tccgctgtgt gttctcttcc aggccagcag
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gagaatcctc ccctgcccct tggctcaaag gtggtggttc tggcggggct gttcgtgatg
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gtgttgatcc tcttcctggg agcctccatg gtntacctga tccgggtngc acggaggaac
                                                                     240
cagggagcgt gccctgcgna ccgtctngga gctccggaga tgacaaggag cagctggtga
                                                                     300
agaacacata tgtcctgtga ccgncctgtt cgncaagagg actnggggaa aggggagggg
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agattatgtg ttgagttttt tttaaantag
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                                                                     120
tggcggggct gttcgtgatg gtgttgatcc tcttcctggg agcctccatg gtctacctga
                                                                     180
                                                                     240
tccgggtggc acggaggaac cagggagcgt gccctgcgca ccgtctggga gctccggaga
tgacaaggga gcagctggtg aagaacacat atgttcctgt tgaccgccct gttcgccaag
                                                                     300
agggantggg ggaaggggag ggggaganta ttgttgttga gnttttttt aaaattagga
                                                                     360
ggggnttgan ttcgggnttt tnagttgatc catttagggg gntgag
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                                                                      60
aaaggtggtg gttctggcgg ggctgttcgt gatggtgttg atcctcttcc tgggagcctc
                                                                     120
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180
catggtctac ctgatccggg tngcacggag gaaccaggag cgtgccctgc gcaccgtctg
gagctccgga gatgacaagg agcagctggt gaagaacaca tatgtcctgt gaccgccctg
                                                                     240
tcgccaagag gactggggaa gggaggggag actatgtgtg agctttttt aaatagaggg
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                                                                     120
aggagcagct ggtgaagaac acatatgtcc tgtgaccgcc ctgtcgccaa gaggactggg
                                                                     180
gaagggaggg gagactatgt gtgagctttt tttaaataga gggattgact cggatttgag
                                                                     240
tgatcattag ggctgaggtc tgtttctctg ggaggtagga cggctgcttc ctgggtcttg
                                                                     300
gcagggatgg ggtttgcttt gggaaatcct cttnggaggc tcctccttcg catgggcctt
                                                                     360
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                                                                    120
tcgcatggcc tgcagtctgg cagcagcccc gagttgttnc ctcgctgatc gatntctttc
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331

180

gaaggaaagt aaaatgtaca agtttaataa a

| ccccaggtag agttttcttt gcttatgttg aantccattg cctcttttct catcacagaa | 240 |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|
| gtgatgttgg aatcgtttct tttgtttgtc tgatttatgg tttttttaag tataaacaaa | 300 |
| agttttttat tagcattctg aaagaaggaa agtaaantgt acaagtttaa taaaaagggg | 360 |
| ccttcccctt taa | 373 |
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| ttcgcatggc ctgcagtctg gcagcagccc cgagttgttt cctcgctgat cgatttcttt | 180 |
| cctccaggta gagttttctt tgcttatgtt gaattccatt gcctcttttc tcatcacaga | 240 |
| agtgatgttg gaatcgtttc ttttgtttgt ctgatttatg gtttttttaa gtataaacaa | 300 |
| aagttttta ttagcattct gaaagaagga aagtaaaatg tacaagttta ataaaaaggg | 360 |
| gccttcccct ttagaataaa | 380 |
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| agtotggcag cagocogagt tgtttcctcg ctgatcgatt totttcctcc aggtagagtt | 120 |
| ttctttgctt atgttgaatt ccattgcctc ttttctcatc acagaagtga tgttggaatc | |
| | 180 |
| gtttcttttg tttgtctgat ttatggtttt tttaagtata aacaaaagtt ttttattagc | 180 240 |

| aatnaaaana aaaaagggtg | | | | | | |
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| ggctgcttca tggtctggca gggatgggtt tgctttggaa atcctctagg aggctcctcc | 120 | | | | | |
| togcatggcc tgcagtctgc agcagccccg agttgtttcc tcgctgatcg atttctttcc | 180 | | | | | |
| tccaggtaga gttttctttg cttatgttga attccattgc ctcttttctc atcacagaag | 240 | | | | | |
| tgatgttgga atcgtttctt ttgtttgtct gatttatggt ttttttaagt ataaacaaaa | 300 | | | | | |
| gttttttatt agcattctga aagaaggaaa gtaaaatgta caagtttaat aaaaaggggc | 360 | | | | | |
| cttccccttt agaataaatt tcagcatgtg ctttcaa | 397 | | | | | |
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| cncatcacag aagtgatgtt ggaatcgttt cttttgtttg tctgatttat ggttttttta | 180 |
| agtntaaaca aaagtttttt attagcattc tgaaagaagg aaagtaaaat gtacaagttt | 240 |
| aataaaaagg ggccttcccc tttagaataa aaaaaaaaaa | 289 |
| <pre><210> 103 <211> 311 <212> DNA <213> Homo sapiens <220> <221> misc_feature <222> (7)(7) <223> "n" is any nucleotide.</pre> | |
| <400> 103 | 60 |
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| gttgtttcct cgctgatcgg atttctttcc tccaggtaga gttttctttg cttatgttga | 120 |
| attccattgc ctcttttctc atcacagaag tgatgttgga atcgtttctt ttgtttgtct | 180 |
| gatttatggt ttttttaagt ataaacaaaa gttttttatt agcattctga aagaaggaaa | 240 |
| gtaaaatgta caagtttaat aaaaaggggc cttccccttt agaataaatt tcagcatgtg | 300 |
| ctttcaaaaa a | 311 |
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| 1 | tgcagtno | ctg | gcagcagacc | ccgagttgtt | tcctcgctga | tcgatttctt | tacccccagg | 120 |
| | tagagttt | ttc (| ctttgnctta | tgttgaattc | cattgcctct | tttactcatc | acagaagtga | 180 |
| | tgttggaa | atc (| gtttcttttg | tttgtctgat | ttatggtttt | tttaagtata | aacaaaagtt | 240 |
| | ttttatta | agc a | attctgaaag | aaggaaagta | aaatgtacaa | gtttaataaa | aaggggcctt | 300 |
| | ccccttta | aga a | ataaaaaaaa | aaaaaaaaa | aaaaaaaa | | | 338 |
| | <220> <221> m <222> (<223> " <220> <221> m <222> (<221> m <222> (<223> " | 343 DNA Homo nisc (13) 'n" nisc (19) | is any nucl _feature (19) is any nucl _feature | eotide. | | | | |
| | | | • | | | | | |
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| | gcatggco | ctg (| cagtctggca | gcagccccga | gttgtttcct | cgctgancga | tttctttcct | 120 |
| | ccaggtag | gag t | tttctttgc | ttatgttgaa | ttccattgcc | tcttttctca | tcacagaagt | 180 |
| | gatgttgg | gaa t | tegtttettt | tgtttgtctg | atttatggtt | tttttaagta | taaacaaaag | 240 |
| | ttttttat | ta 🤉 | gcattctgaa | agaaggaaag | taaaatgtac | aagtttaata | aaaaggggcc | 300 |
| | ttcccctt | ta 🤉 | gaataaaaaa | aaaaaaaaaa | aaaaaaaaa | aaa | | 343 |
| | | | | | | | | |